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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/087,137

DATE: 03/19/2002

TIME: 16:00:18

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J087137.raw

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3 <110> APPLICANT: Dederer, Douglas
4     Yamazaki, Victoria
5     Asundi, Vinod
6     Liu, Chenghua
7     Tang, Y. Tom
8     Drmanac, Radoje T.
10 <120> TITLE OF INVENTION: Methods of Therapy and Diagnosis Using Insulin-like Growth
Factor Binding
11     Protein-like Polypeptides and Polynucleotides
13 <130> FILE REFERENCE: HYS-38CIP
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/087,137
16 <141> CURRENT FILING DATE: 2002-02-27
18 <150> PRIOR APPLICATION NUMBER: 09/784,748
19 <151> PRIOR FILING DATE: 2001-02-14
21 <150> PRIOR APPLICATION NUMBER: 09/649,167
22 <151> PRIOR FILING DATE: 2000-08-23
24 <150> PRIOR APPLICATION NUMBER: 09/540,217
25 <151> PRIOR FILING DATE: 2000-03-31
27 <160> NUMBER OF SEQ ID NOS: 14
29 <170> SOFTWARE: PatentIn version 3.1
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32 <211> LENGTH: 375
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41 tcaccggggc gcaggtgggc ctgtcctgtg aagtgcgggc tgtgcctacc ccagtcacga      180
43 cgtggagaaa ggtcacgaag tcccctgagg gcacccaagc actggaggag ctgcctgggg      240
45 accatgtcaa tatagctgtc caagtgcgag ggggcccttc tgaccatgag gccacggcct      300
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62 atgttctaag tcattttcag tattttacac ccatgttacg agatatttga ggtggcttat      180
64 aagacctgta gaaaaagaaa gaaaaatacg taaatggagg aaaccaggga aagagcaaaa      240
66 gaagagtagg gacatactta gatgagcagt agaatccctg gtatattctg cacacatctc      300
68 cctctgagct tcttagcatg caaagacaag agctgtgaac atgaagggtg gtccatgaga      360
70 tgaaaagacc agttgtgttt tggggctgga gggaatattt cctctgtatt cttttagaaa      420

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85 tcaccggggc gcaggtgggc ctgtcctgtg aagtgcgggc tgtgcctacc ccagtcata 180
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89 accatgtcaa tatagctgtc caagtgcgag ggggcccttc tgaccatgag gccacggcct 300
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114 ccgctggggc agcgcgcgag ggcaccgggc tctgcgtgtg cgcgcagcgc ggcaccgtct 420
116 gcggctccga cggctcgtcg taccacagcg tctgcgcgct gcgcctgcgc gctcggcaca 480
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140 ccacctactc ctactccagc accctttctc cttcacaggt gtttctccta atacatctct 1200
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160	Met Pro Arg Leu Ser Leu Leu Leu Pro Leu Leu	
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163	ctt ctg ctg ctg ctg ccg ctg ctg ccg ccg ctg tcc ccg agc ctc ggg	159
164	Leu Leu Leu Leu Leu Pro Leu Leu Pro Pro Leu Ser Pro Ser Leu Gly	
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167	atc cgc gac gtg ggc ggc cgc cgc ccc aag tgt ggt ccg tgc cgg cca	207
168	Ile Arg Asp Val Gly Gly Arg Arg Pro Lys Cys Gly Pro Cys Arg Pro	
169	30 35 40	
171	gag ggc tgc ccg gcg cct gcg ccc tgc ccg gcg ccc ggg atc tcg gcg	255
172	Glu Gly Cys Pro Ala Pro Ala Pro Cys Pro Ala Pro Gly Ile Ser Ala	
173	45 50 55	
175	ctc gac gag tgc ggc tgc tgc gcc cgc tgc ctg gga gcc gag ggc gcg	303
176	Leu Asp Glu Cys Gly Cys Cys Ala Arg Cys Leu Gly Ala Glu Gly Ala	
177	60 65 70 75	
179	agc tgc ggg ggc cgc gcc ggc ggc cgc tgt ggc ccc ggc ctg gta tgc	351
180	Ser Cys Gly Gly Arg Ala Gly Gly Arg Cys Gly Pro Gly Leu Val Cys	
181	80 85 90	
183	gcg agc cag gcc gct ggg gca gcg ccc gag ggc acc ggg ctc tgc gtg	399
184	Ala Ser Gln Ala Ala Gly Ala Ala Pro Glu Gly Thr Gly Leu Cys Val	
185	95 100 105	
187	tgc gcg cag cgc ggc acc gtc tgc ggc tcc gac ggt cgc tcg tac ccc	447
188	Cys Ala Gln Arg Gly Thr Val Cys Gly Ser Asp Gly Arg Ser Tyr Pro	
189	110 115 120	
191	agc gtc tgc gcg ctg cgc ctg cgc gct ccg cac acg ccc cgc gcg cac	495
192	Ser Val Cys Ala Leu Arg Leu Arg Ala Arg His Thr Pro Arg Ala His	
193	125 130 135	
195	ccc ggt cac ctg cac aag gcg cgc gac ggc cct tgc gag ttc gct cct	543
196	Pro Gly His Leu His Lys Ala Arg Asp Gly Pro Cys Glu Phe Ala Pro	
197	140 145 150 155	
199	gtg gtc gtc gtt cct ccc cga agt gtt cac aac gtc acc ggg gcg cag	591
200	Val Val Val Val Pro Pro Arg Ser Val His Asn Val Thr Gly Ala Gln	
201	160 165 170	
203	gtg ggc ctg tcc tgt gaa gtg agg gct gtg cct acc cca gtc atc acg	639
204	Val Gly Leu Ser Cys Glu Val Arg Ala Val Pro Thr Pro Val Ile Thr	
205	175 180 185	
207	tgg aga aag gtc acg aag tcc cct gag ggc acc caa gca ctg gag gag	687
208	Trp Arg Lys Val Thr Lys Ser Pro Glu Gly Thr Gln Ala Leu Glu Glu	
209	190 195 200	
211	ctg cct ggg gac cat gtc aat ata gct gtc caa gtg cga ggg ggc cct	735
212	Leu Pro Gly Asp His Val Asn Ile Ala Val Gln Val Arg Gly Gly Pro	
213	205 210 215	
215	tct gac cat gag gcc acg gcc tgg att ttg atc aac ccc ctg cga aag	783
216	Ser Asp His Glu Ala Thr Ala Trp Ile Leu Ile Asn Pro Leu Arg Lys	
217	220 225 230 235	
219	gag gat gag ggt gtg tac cag tgc cat gca gcc aac atg gtg gga gag	831
220	Glu Asp Glu Gly Val Tyr Gln Cys His Ala Ala Asn Met Val Gly Glu	
221	240 245 250	
223	gct gag tcc cac agc aca gtg acg gtt cta gat ctg agt aaa tac agg	879

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228 Ser Phe His Phe Pro Ala Pro Asp Asp Arg Met
229                270                275
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237 <211> LENGTH: 278
238 <212> TYPE: PRT
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 6
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248                20                25                30
251 Gly Arg Arg Pro Lys Cys Gly Pro Cys Arg Pro Glu Gly Cys Pro Ala
252                35                40                45
255 Pro Ala Pro Cys Pro Ala Pro Gly Ile Ser Ala Leu Asp Glu Cys Gly
256                50                55                60
259 Cys Cys Ala Arg Cys Leu Gly Ala Glu Gly Ala Ser Cys Gly Gly Arg
260 65                70                75                80
263 Ala Gly Gly Arg Cys Gly Pro Gly Leu Val Cys Ala Ser Gln Ala Ala
264                85                90                95
267 Gly Ala Ala Pro Glu Gly Thr Gly Leu Cys Val Cys Ala Gln Arg Gly
268                100               105               110
271 Thr Val Cys Gly Ser Asp Gly Arg Ser Tyr Pro Ser Val Cys Ala Leu
272                115               120               125
275 Arg Leu Arg Ala Arg His Thr Pro Arg Ala His Pro Gly His Leu His
276                130               135               140
279 Lys Ala Arg Asp Gly Pro Cys Glu Phe Ala Pro Val Val Val Val Pro
280 145               150               155               160
283 Pro Arg Ser Val His Asn Val Thr Gly Ala Gln Val Gly Leu Ser Cys
284                165               170               175
287 Glu Val Arg Ala Val Pro Thr Pro Val Ile Thr Trp Arg Lys Val Thr
288                180               185               190
291 Lys Ser Pro Glu Gly Thr Gln Ala Leu Glu Glu Leu Pro Gly Asp His
292                195               200               205
295 Val Asn Ile Ala Val Gln Val Arg Gly Gly Pro Ser Asp His Glu Ala
296                210               215               220
299 Thr Ala Trp Ile Leu Ile Asn Pro Leu Arg Lys Glu Asp Glu Gly Val
300 225               230               235               240
303 Tyr Gln Cys His Ala Ala Asn Met Val Gly Glu Ala Glu Ser His Ser
304                245               250               255
307 Thr Val Thr Val Leu Asp Leu Ser Lys Tyr Arg Ser Phe His Phe Pro
308                260               265               270
311 Ala Pro Asp Asp Arg Met
312                275
315 <210> SEQ ID NO: 7

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RAW SEQUENCE LISTING

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325 tgccggccag agggctgccc ggcgcctgcg cctgccccgg cgcccgggat ctgggcgctc      180
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331 gagggcaccg ggctctgcgt gtgcgcgcag cgcggcaccg tctgcggctc cgacggctgc      360
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339 gtgcctaccc cagtcatcac gtggagaaag gtcacgaagt cccctgaggg cacccaagca      600
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343 gaccatgagg ccacggcctg gattttgatc aacccccctgc gaaaggagga tgagggtgtg      720
345 taccagtgcc atgcagccaa catggtggga gaggtgagt cccacagcac agtgacggtt      780
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373          20          25
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377 <211> LENGTH: 251
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379 <213> ORGANISM: Homo sapiens
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392          35          40          45
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396          50          55          60
399 Ala Ser Gln Ala Ala Gly Ala Ala Pro Glu Gly Thr Gly Leu Cys Val
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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
